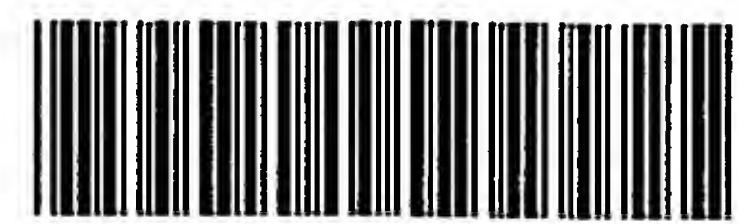


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/594,117
Source: IFWP
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IFWP

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PATENT APPLICATION: US/10/594,117

DATE: 10/06/2006

TIME: 11:10:29

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3 <110> APPLICANT: Golz, Stefan
 4 Bruggemeier, Ulf
 5 Geerts, Andreas
 6 Summer, Holger
 8 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with Protein
 9 Kinase, cGMP-Dependent, Type I (PRKG1)
 11 <130> FILE REFERENCE: 004974.01219
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/594,117
 C--> 12 <141> CURRENT FILING DATE: 2006-09-25
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/02531
 13 <151> PRIOR FILING DATE: 2005-03-10
 15 <150> PRIOR APPLICATION NUMBER: EP 04007085.6
 16 <151> PRIOR FILING DATE: 2004-03-24
 18 <160> NUMBER OF SEQ ID NOS: 5
 20 <170> SOFTWARE: PatentIn version 3.2
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 23 <211> LENGTH: 3740
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 29 gggcaccttgcggattttac agtacgcgct ccaggagaag atcgaggagc tgaggcagcg 120
 30 ggatgtctc atcgacgagc tggagcttggaa gttggatcg aaggacgaac tgatccagaa 180
 31 gctgcagaac gagctggaca agtaccgctc ggtgatccga ccagccaccc agcaggcgca 240
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 33 cgagccaccgccttcgaca tccaggatct cagccatgtg accctgcctt tctaccccaa 360
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 35 cttggagctg tcgcagatcc aggagattgt ggattgtatg taccctggatgg agtatggcaa 480
 36 ggacagttgc atcatcaaag aaggagacgt ggggtcactg gtgtatgtca tggaagatgg 540
 37 taaggttcaa gttacaaaag aaggtgttcaa gttgttacc atgggtccag gaaaagtgtt 600
 38 tggggatttgcatttataactgtac ccggacagcg accgtcaaga ctcttgtaaa 660
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 41 tgaagagatc ctcagcaagc ttgttgcatttataactgtac ccggacagcg accgtcaaga 840
 42 atatattatc aggcaaggttgcatttataactgtac ccggacagcg accgtcaaga 900
 43 aaatgttact cgttgcatttataactgtac ccggacagcg accgtcaaga 960
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 48 tggagtttgcatttataactgtac ccggacagcg accgtcaaga 1260
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 52 ctggaccatt ctcagggata gaggttcgtt tgaagattct acaaccagat ttacacacgc 1500
 53 atgtgtggta gaagctttg cctatctgca ttccaaagga atcattaca gggacctcaa 1560
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 55 aaagaaaaata ggatttgaa agaaaacatg gactttgt gggactccag agtatgtagc 1680
 56 cccagagatc atcctgaaca aaggccatga catttcagcc gactactggt cactggaaat 1740
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 58 ctataacatc atattgaggg ggattgacat gatagaattt ccaaagaaga ttgccaaaaaa 1860
 59 tgctgctaattttaattaaaaa aactatgcag ggacaatcca tcagaaagat taggaaattt 1920
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 78 tattccctt tataaaaaata aatgcttggg gtagggtgga gtggggaggg attaaaaccc 3060
 79 atccaaaaaaaaaa taaataaaaaa ctatataatgtt gctatgtata tctttcatct gtaaatgtca 3120
 80 gtgtctgaaac agcaacacaa attcaaatca ttatacgtt agccagaaac tcaagcattt 3180
 81 tcactaaatgttattaaacca aactcctgtc caatttgact tatacaacat agtcagtcta 3240
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 83 accaaaaaaaaac aacaaacaaa caaaaaacaa gaataaaaaa cagaaataaa agaagttagaa 3360
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 89 ggagaaaaaga atccacaaat taaactgagt cttcactgg catgccagtt gactattatt 3720
 90 agctgtcata agtaaccccg 3740
 92 <210> SEQ ID NO: 2
 93 <211> LENGTH: 686
 94 <212> TYPE: PRT
 95 <213> ORGANISM: Homo sapiens
 97 <400> SEQUENCE: 2
 98 Met Gly Thr Leu Arg Asp Leu Gln Tyr Ala Leu Gln Glu Lys Ile Glu
 99 1 5 10 15
 100 Glu Leu Arg Gln Arg Asp Ala Leu Ile Asp Glu Leu Glu Leu Glu Leu
 101 20 25 30

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103      35          40          45
104 Tyr Arg Ser Val Ile Arg Pro Ala Thr Gln Gln Ala Gln Lys Gln Ser
105      50          55          60
106 Ala Ser Thr Leu Gln Gly Glu Pro Arg Thr Lys Arg Gln Ala Ile Ser
107 65      70          75          80
108 Ala Glu Pro Thr Ala Phe Asp Ile Gln Asp Leu Ser His Val Thr Leu
109      85          90          95
110 Pro Phe Tyr Pro Lys Ser Pro Gln Ser Lys Asp Leu Ile Lys Glu Ala
111      100         105         110
112 Ile Leu Asp Asn Asp Phe Met Lys Asn Leu Glu Leu Ser Gln Ile Gln
113      115         120         125
114 Glu Ile Val Asp Cys Met Tyr Pro Val Glu Tyr Gly Lys Asp Ser Cys
115      130         135         140
116 Ile Ile Lys Glu Gly Asp Val Gly Ser Leu Val Tyr Val Met Glu Asp
117 145      150         155         160
118 Gly Lys Val Glu Val Thr Lys Glu Gly Val Lys Leu Cys Thr Met Gly
119      165         170         175
120 Pro Gly Lys Val Phe Gly Glu Leu Ala Ile Leu Tyr Asn Cys Thr Arg
121      180         185         190
122 Thr Ala Thr Val Lys Thr Leu Val Asn Val Lys Leu Trp Ala Ile Asp
123      195         200         205
124 Arg Gln Cys Phe Gln Thr Ile Met Met Arg Thr Gly Leu Ile Lys His
125      210         215         220
126 Thr Glu Tyr Met Glu Phe Leu Lys Ser Val Pro Thr Phe Gln Ser Leu
127 225      230         235         240
128 Pro Glu Glu Ile Leu Ser Lys Leu Ala Asp Val Leu Glu Glu Thr His
129      245         250         255
130 Tyr Glu Asn Gly Glu Tyr Ile Ile Arg Gln Gly Ala Arg Gly Asp Thr
131      260         265         270
132 Phe Phe Ile Ile Ser Lys Gly Thr Val Asn Val Thr Arg Glu Asp Ser
133      275         280         285
134 Pro Ser Glu Asp Pro Val Phe Leu Arg Thr Leu Gly Lys Gly Asp Trp
135      290         295         300
136 Phe Gly Glu Lys Ala Leu Gln Gly Glu Asp Val Arg Thr Ala Asn Val
137 305      310         315         320
138 Ile Ala Ala Glu Ala Val Thr Cys Leu Val Ile Asp Arg Asp Ser Phe
139      325         330         335
140 Lys His Leu Ile Gly Gly Leu Asp Asp Val Ser Asn Lys Ala Tyr Glu
141      340         345         350
142 Asp Ala Glu Ala Lys Ala Lys Tyr Glu Ala Glu Ala Ala Phe Phe Ala
143      355         360         365
144 Asn Leu Lys Leu Ser Asp Phe Asn Ile Ile Asp Thr Leu Gly Val Gly
145      370         375         380
146 Gly Phe Gly Arg Val Glu Leu Val Gln Leu Lys Ser Glu Glu Ser Lys
147 385      390         395         400
148 Thr Phe Ala Met Lys Ile Leu Lys Lys Arg His Ile Val Asp Thr Arg
149      405         410         415
150 Gln Gln Glu His Ile Arg Ser Glu Lys Gln Ile Met Gln Gly Ala His

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|-----|---|-----|-----|
| 151 | 420 | 425 | 430 |
| 152 | Ser Asp Phe Ile Val Arg Leu Tyr Arg Thr Phe Lys Asp Ser Lys Tyr | | |
| 153 | 435 | 440 | 445 |
| 154 | Leu Tyr Met Leu Met Glu Ala Cys Leu Gly Gly Glu Leu Trp Thr Ile | | |
| 155 | 450 | 455 | 460 |
| 156 | Leu Arg Asp Arg Gly Ser Phe Glu Asp Ser Thr Thr Arg Phe Tyr Thr | | |
| 157 | 465 | 470 | 475 |
| 158 | 480 | 485 | 495 |
| 159 | Ala Cys Val Val Glu Ala Phe Ala Tyr Leu His Ser Lys Gly Ile Ile | | |
| 160 | Tyr Arg Asp Leu Lys Pro Glu Asn Leu Ile Leu Asp His Arg Gly Tyr | | |
| 161 | 500 | 505 | 510 |
| 162 | Ala Lys Leu Val Asp Phe Gly Phe Ala Lys Lys Ile Gly Phe Gly Lys | | |
| 163 | 515 | 520 | 525 |
| 164 | Lys Thr Trp Thr Phe Cys Gly Thr Pro Glu Tyr Val Ala Pro Glu Ile | | |
| 165 | 530 | 535 | 540 |
| 166 | Ile Leu Asn Lys Gly His Asp Ile Ser Ala Asp Tyr Trp Ser Leu Gly | | |
| 167 | 545 | 550 | 555 |
| 168 | 560 | 565 | 575 |
| 169 | Ile Leu Met Tyr Glu Leu Leu Thr Gly Ser Pro Pro Phe Ser Gly Pro | | |
| 170 | 580 | 585 | 590 |
| 171 | Asp Pro Met Lys Thr Tyr Asn Ile Ile Leu Arg Gly Ile Asp Met Ile | | |
| 172 | 595 | 600 | 605 |
| 173 | Glu Phe Pro Lys Lys Ile Ala Lys Asn Ala Ala Asn Leu Ile Lys Lys | | |
| 174 | 610 | 615 | 620 |
| 175 | Val Lys Asp Ile Gln Lys His Lys Trp Phe Glu Gly Phe Asn Trp Glu | | |
| 176 | 625 | 630 | 635 |
| 177 | 640 | 645 | 655 |
| 178 | Gly Leu Arg Lys Gly Thr Leu Thr Pro Pro Ile Ile Pro Ser Val Ala | | |
| 179 | 660 | 665 | 670 |
| 180 | Ser Pro Thr Asp Thr Ser Asn Phe Asp Ser Phe Pro Glu Asp Asn Asp | | |
| 181 | 675 | 680 | 685 |
| 182 | Glu Pro Pro Pro Asp Asp Asn Ser Gly Trp Asp Ile Asp Phe | | |
| 183 | 690 | 695 | 700 |
| 185 | <210> SEQ ID NO: 3 | | |
| 186 | <211> LENGTH: 20 | | |
| 187 | <212> TYPE: DNA | | |
| 188 | <213> ORGANISM: artificial sequence | | |
| 190 | <220> FEATURE: | | |
| 191 | <223> OTHER INFORMATION: forward primer | | |
| 193 | <400> SEQUENCE: 3 | | |
| 194 | agccgactac tggcactgg | | 20 |
| 196 | <210> SEQ ID NO: 4 | | |
| 197 | <211> LENGTH: 20 | | |
| 198 | <212> TYPE: DNA | | |
| 199 | <213> ORGANISM: artificial sequence | | |
| 201 | <220> FEATURE: | | |
| 202 | <223> OTHER INFORMATION: reverse primer | | |
| 204 | <400> SEQUENCE: 4 | | |
| 205 | gatctgggcc tgagaaagggt | | 20 |

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210 <213> ORGANISM: artificial sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: probe
215 <400> SEQUENCE: 5
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25

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/594,117

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date